PATENT
Attorney Docket Number: 2356.0062-05

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

ASSISTANT COMMISSIONER FOR PATENTS
Washington, D.C. 20231

Prior Application: Art Unit: 1648

Examiner: J. Stucker

SIR: This is a request for filing a

☒ Continuation ☐ Continuation-in-Part ☐ Divisional Application under 37 C.F.R. § 1.53(b) of pending prior application Serial No. 09/092,077 filed June 5,1998 of Maurice MONCANY and Luc MONTAGNIER for NUCLEOTIDE SEQUENCES DERIVED FROM THE GENOME OF RETROVIRUSES OF THE HIV-1, HIV-2 AND SIV TYPE, AND THEIR USES IN PARTICULAR FOR THE AMPLIFICATION OF THE GENOMES OF THESE RETROVIRUSES AND FOR THE IN VITRO DIAGNOSIS OF THE DISEASES DUE TO THESE VIRUSES.

1. ☒ Enclosed is a complete copy of the prior application including the oath or Declaration and drawings, if any, as originally filed. I hereby verify that the attached papers are a true copy of prior application Serial No. 09/092,077 as originally filed on June 5, 1998.

2. ☐ Enclosed is a substitute specification under 37 C.F.R. § 1.125.

3. ☐ Cancel Claims _____.

4. ☒ A Preliminary Amendment is enclosed.

5. ☒ The filing fee is calculated on the basis of the claims existing in the prior application as amended at 3 and 4 above.

Basic Application Filing Fee					$690.00	$ $690.00
	Number of Claims		Basic	Extra Claims		
Total Claims	10	-	20	0	X $18	0.00
Independent Claims	2	-	3	0	X $78	0.00
☒ Presentation of Multiple Dep. Claim(s)					+$260	260.00
Subtotal						$ 950.00
Reduction by 1/2 if small entity						- 0.00
TOTAL APPLICATION FILING FEE						$ 950.00

6. ☒ A check in the amount of $950.00 to cover the filing fee is enclosed.

7. ☒ The Commissioner is hereby authorized to charge any fees which may be required including fees due under 37 C.F.R. § 1.16 and any other fees due under 37 C.F.R. § 1.17, or credit any overpayment during the pendency of this application to Deposit Account No. 06-0916.

8. ☒ Amend the specification by inserting before the first line, the sentence:

--This is a ☒ continuation ☐ division of application Serial No.09/092,077, filed June 5, 1998, which is a division of application Serial No. 08/895,231, filed July 16, 1997, which is a division of 08/160,465, filed December 2, 1993, which is a continuation of application Serial No. 07/820,599, filed January 21, 1992, all of which is incorporated herein by reference.--

9. ☐ New formal drawings are enclosed.

10. ☒ The prior application is assigned of record to: Institut Pasteur and Institut National de la Sante et de la Recherche Medicale.

11. ☒ Priority of application Serial No. PCT/FR90/0393, filed May 6, 1990 in , filed in France; application Serial No. FR89/07354, filed June 2, 1989; and application Serial No. FR89/12371, filed September 20, 1989 is claimed under 35 U.S.C. § 119. Certified copies

☐ is enclosed or ☒ are on file in the prior application.

12. ☐ A verified statement claiming small entity status

☐ is enclosed or ☐ is on file in the prior application.

13. ☒ The power of attorney in the prior application is to at least one of the following: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P., Douglas B. Henderson, Reg. No. 20,291; Ford F. Farabow, Jr., Reg. No. 20,630; Arthur S. Garrett, Reg. No. 20,338; Donald R. Dunner, Reg. No. 19,073; Brian G. Brunsvold, Reg. No. 22,593; Tipton D. Jennings, IV, Reg. No. 20,645; Jerry D. Voight, Reg. No. 23,020; Laurence R. Hefter, Reg. No. 20,827; Kenneth E. Payne, Reg. No. 23,098; Herbert H. Mintz, Reg. No. 26,691; C. Larry O'Rourke, Reg. No. 26,014; Albert J. Santorelli, Reg. No. 22,610; Michael C. Elmer, Reg. No. 25,857; Richard H. Smith, Reg. No. 20,609; Stephen L. Peterson, Reg. No. 26,325; John M. Romary, Reg. No. 26,331; Bruce C. Zotter, Reg. No. 27,680; Dennis P. O'Reilley, Reg. No. 27,932; Allen M. Sokal,

Reg. No. 26,695; Robert D. Bajefsky, Reg. No. 25,387; Richard L. Stroup, Reg. No. 28,478; David W. Hill, Reg. No. 28,220; Thomas L. Irving, Reg. No. 28,619; Charles E. Lipsey, Reg. No. 28,165; Thomas W. Winland, Reg. No. 27,605; Basil J. Lewris, Reg. No. 28,818; Martin I. Fuchs, Reg. No. 28,508; E. Robert Yoches, Reg. No. 30,120; Barry W. Graham, Reg. No. 29,924; Susan Haberman Griffen, Reg. No. 30,907; Richard B. Racine, Reg. No. 30,415; Thomas H. Jenkins, Reg. No. 30,857; Robert E. Converse, Jr., Reg. No. 27,432; Clair X. Mullen, Jr., Reg. No. 20,348; Christopher P. Foley, Reg. No. 31,354; John C. Paul, Reg. No. 30,413; David M. Kelly, Reg. No. 30,953; Kenneth J. Meyers, Reg. No. 25,146; Carol P. Einaudi, Reg. No. 32,220; Walter Y. Boyd, Jr., Reg. No. 31,738; Steven M. Anzalone, Reg. No. 32,095; Jean B. Fordis, Reg. No. 32,984; Roger D. Taylor, Reg. 28,992; Barbara C. McCurdy, Reg. No. 32,120; James K. Hammond, Reg. No. 31,964; Richard V. Burgujian, Reg. No. 31,744; J. Michael Jakes, Reg. No. 32,824; Thomas W. Banks, Reg. No. 32,719; Christopher P. Isaac, Reg. No. 32,616; Bryan C. Diner, Reg. No. 32,409; M. Paul Barker, Reg. No. 32,013; Andrew Chanho Sonu, Reg. No. 33,457; David S. Forman, Reg. No. 33,694; Vincent P. Kovalick, Reg. No. 32,867; James W. Edmondson, Reg. No. 33,871; Michael R. McGurk, Reg. No. 32,045; Joann M. Neth, Reg. No. 36,363; Gerson S. Panitch, Reg. No. 33,751; Cheri M. Taylor, Reg. No. 33,216; Charles E. Van Horn, Reg. No. 40,266; Linda A. Wadler, Reg. No. 33,218; Jeffrey A. Berkowitz, Reg. No. 36,743; Michael R. Kelly, Reg. No. 33, 921; James B. Monroe, Reg. No. 33,971; Doris Johnson Hines, Reg. No. 34,629; Allen R. Jensen, Reg. No. 28,224; Lori Ann Johnson, Reg. No. 34,498; David A. Manspeizer, Reg. No. 37,540; and Timothy B. Donaldson, Reg. No. 43,592.

14. ☐ The power appears in the original declaration of the prior application.

15. ☐ Since the power does not appear in the original declaration, a copy of the power in the prior application is enclosed.

16. ☒ Please address all correspondence to FINNEGAN, HENDERSON, FARABOW, GARRETT and DUNNER, L.L.P., 1300 I Street, N.W., Washington, D.C. 20005-3315.

17. ☐ Recognize as associate attorney _____

_____

18. ☒ Also enclosed is an Information Disclosure Statement; PTO Form 1449; Statement to Support Filing and Submission In Accordance With 37 C.F.R. §§ 1.821-1.825; and Sequence Listing.

PETITION FOR EXTENSION. If any extension of time is necessary for the filing of this application, including any extension in the parent application, serial no.09/060,756 filed April 16, 1998, for the purpose of maintaining copendency between the parent application and this application, and such extension has not otherwise been requested, such an extension is hereby requested, and the Commissioner is authorized to charge necessary fees for such an extension to our Deposit Account No. 06-0916. A duplicate copy of this paper is enclosed for use in charging the deposit account.

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

Dated: September 26, 2000

By: ________________
Timothy B. Donaldson
Reg. No. 43,592

PATENT
Attorney Docket No. 2356.0062-05

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Rule 1.53(b) cont. appln of: U.S. Serial No. 09/092,077	)	
Maurice MONCANY et al.	)	
Serial No.: Unassigned	)	Prior Group Art Unit: 1648
Filed: September 26, 2000	)	Prior Examiner: J. Stucker

For: NUCLEOTIDE SEQUENCES DERIVED FROM THE GENOME OF RETROVIRUSES OF THE HIV-1, HIV-2 AND SIV TYPE, AND THEIR USES IN PARTICULAR FOR THE AMPLIFICATION OF THE GENOMES OF THESE RETROVIRUSES AND FOR THE IN VITRO DIAGNOSIS OF THE DISEASES DUE TO THESE VIRUSES

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

PRELIMINARY AMENDMENT

Prior to the examination of the above application, please amend this application as follows:

IN THE SPECIFICATION:

Page 6, line 1, after "GAC" insert --(SEQ ID NO:1)--;

line 2, after ". . .", last occurrence, insert --SEQ ID NO:2)--;

line 4, after "AAA A", insert --(SEQ ID NO:3)--;

line 5, after ". . .", last occurrence, insert --SEQ ID NO:4);

line 6, after ". . .", last occurrence, insert--(SEQ ID NO:5)--;

line 8, after "TTT TA" insert --(SEQ ID NO:6)--;

line 9, after ". . .", last occurrence, insert--(SEQ ID NO:7)--;

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line 11, after "TGA TG" insert –(SEQ ID NO:8)--;

line 12, after "G . . ." insert --(SEQ ID NO:9)--;

line 14, after "TGA TG" insert --(SEQ ID NO:10)--;

line 15, after "G . . ." insert --(SEQ ID NO:11)--;

line 18, after "CAA AG" insert --(SEQ ID NO:12)--;

line 19, after "G . . ." insert --(SEQ ID NO:13)--;

line 22, after "GTG G" insert --(SEQ ID NO:14)--;

line 23, after ". . ." insert --(SEQ ID NO:15)--;

line 26, after "CCC T" insert --(SEQ ID NO:16)--;

line 27, after ". . ." insert --(SEQ ID NO:17)--;

line 28, after ". . ." insert --(SEQ ID NO:18)--; and

line 32, after "CAG" insert --(SEQ ID NO:19)--.

Page 7, line 1, after "CTG T" insert --(SEQ ID NO:20)--;

line 5, after "CAA" insert --(SEQ ID NO:21)--;

line 6, after ". . .", last occurrence, insert --(SEQ ID NO:22)--;

line 9, after "TTA" insert --(SEQ ID NO:23)--;

line 10, after ". . .", last occurrence, insert --(SEQ ID NO:24)--;

line 13, after "CAG AA" insert --(SEQ ID NO:25)--;

line 14, after ". . ." insert --(SEQ ID NO:26)--;

line 17, after "GTC CA" insert --(SEQ ID NO:27)--;

line 18, after ". . ." insert --(SEQ ID NO:28)--;

line 21, after "AAG G" insert --(SEQ ID NO:29)--;

line 24, after "CAT G" insert --(SEQ ID NO:30)--;

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line 27, after "GCA GT" insert --(SEQ ID NO:31)--;

line 28, after ". . ." insert --(SEQ ID NO:32)--;

line 31, after "TTC CA" insert --SEQ ID NO:33)--;

line 32, after ". . ." insert --(SEQ ID NO:34)--; and

line 33, after ". . ." insert --(SEQ ID NO:35)--.

Page 8, line 8, after "GTG" insert --(SEQ ID NO.36)--;

line 10, after "GG" insert --(SEQ ID NO.37)--;

line 12, after "TAT AT" insert --(SEQ ID NO.38)--;

line 14, after "CCA" insert --(SEQ ID NO:39)--;

line 20, after "AGT" insert --(SEQ ID NO:40)--;

line 22, after "CTT T" insert --(SEQ ID NO:41)--;

line 24, after "GCT A" insert --(SEQ ID NO:42)--;

line 26, after "GTA A" insert --(SEQ ID NO:43)--;

line 31, after "GAG A" insert --(SEQ ID NO:44)--; and

line 34, after "GGA" insert --(SEQ ID NO:45)--.

Page 9, line 8, after "GCC CC" insert --(SEQ ID NO:46)--;

line 10, after "Mmy5" insert --a-- and after "ATT GG" insert --(SEQ ID NO:47)--;

line 12, after GAA GA" insert --(SEQ ID NO:48)--;

line 14, after "AAT T" insert --(SEQ ID NO:49)--;

line 16, after "GGA T" insert --(SEQ ID NO:50)--;

line 18, after "AAC CC" insert --(SEQ ID NO:51)--;

line 20, after "AGC AC" insert --(SEQ ID NO:52)--;

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line 22, after "AGT AG" insert --(SEQ ID NO:53)--;

line 23, after ". . . ." insert --(SEQ ID NO:68)--;

line 25, after "CCC AT" inset --(SEQ ID NO:54)--;

line 27, after "GTG G" insert --(SEQ ID NO:55)--;

line 29, after "TGA A" insert --(SEQ ID NO:56)--; and

line 31, after "CTG G" insert --(SEQ ID NO:57)--.

Page 10, line 1, after "GGA" insert --(SEQ ID NO:58)--;

line 3, after "TCT TTT" insert --(SEQ ID NO:59)--;

line 6, after "TCC C" insert --(SEQ ID NO:60)--;

line 10, after "GTT GAT" insert --(SEQ ID NO:61)--;

line 12, after "CTG TA" insert --(SEQ ID NO:62)--;

line 14, after "TCT GC" insert --(SEQ ID NO:63)--;

line 16, after "CTC TA" insert --(SEQ ID NO:64)--;

line 20, after "ACC T" insert --(SEQ ID NO:65)--;

line 22, after "TGA GAG" insert --(SEQ ID NO:66)--; and

line 24, after "CCA AA" insert --(SEQ ID NO:67)--.

After page 28 insert the attached Sequence Listing pages.

IN THE CLAIMS:

Please cancel claims 1-26.

Please add the following new claims.

--27. A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

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a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

nucleotides 6905-6930, 7055-7077, 7360-7384, 7832-7857, 8844-8869, 7629-7647, and 8224-8242 of the *env* gene of HIV-1 Bru;

nucleotides 6930-6905, 7384-7360, 7857-7832, 8869-8844, and nucleotides 8242-8224 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928, 7053-7075, 7349-7373, 7821-7846, 7612-7630, 8213-8231, and 8836-8861 of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903, 7373-7349, 7846-7821, 8861-8836, and 8231-8213 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885, 7010-7032, 7306-7330, 7775-7800, 8787-8812, 7572-7590, and 8167-8185 of the *env* gene of HIV-1 Eli; and

nucleotides 6885-6860, 7330-7306, 7800-7775, 8812-8787, and 8185-8167 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

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d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

28. A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);

MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);

MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);

MMy7: ATC CTC A0G AGG GGA CCC AGA AAT T (SEQ ID NO:49);

MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);

MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);

MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

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MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56); and

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57);

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

29. An antibody capable of binding to the polypeptide of claims 27 or 28.

30. A method for the *in vitro* diagnosis of the infection of a mammal by a virus of the HIV-1, HIV-2, or SIV type, said virus comprising at least one polypeptide antigen, said method comprising placing a biological sample taken from said mammal in contact with antibody according to claim 29, and detecting the immunological complex formed between said antigen and said antibody.

31. A kit for the diagnosis of infection of a mammal by a virus of the HIV-1, HIV-2, or SIV type, said kit comprising an antibody according to claim 29 and reagents for the detection of the immunological complex formed between said antibody and said antigen.

32. A composition comprising at least one polypeptide according to claim 27 in combination with a pharmaceutically acceptable vehicle.

33. A composition comprising at least one polypeptide according to claim 28 in combination with a pharmaceutically acceptable vehicle.--

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REMARKS

Claims 1-26 have been canceled. Claims 27-33 have been added and are the only claims pending. Claims 27-33 are supported by original claims 1-26. Additional support for the term "fragment" in claims 27 and 28 can be found in the specification, including, for example, at pages 3-4 and 17, which explain that the nucleic acid molecules of the invention include fragments of the full length sequences of various viral genes. For example, the specification states that the nucleotide sequences of the invention "are contained in one of the nucleotide sequences included in [various viral] genes . . . ." (Specification, pages 3-4.) Similarly, as explained in the specification, Tables I to XI represent the size of numerous nucleotide **fragments** generated by amplifying genomic DNA with assorted pairs of primers according to the invention. (Specification, page 17.) If the specification describes nucleotide fragments of various viral genes, it follows that translation of these nucleotide fragments will yield polypeptide fragments of the corresponding viral proteins. (Specification, page 26.) Thus, no new matter has been added.

Sequence Listing

Applicants declare that the computer readable form in this application is identical with that filed in application Serial No. 08/472,928, (hereinafter "the '928 application"). Therefore, applicants request, in accordance with 37 C.F.R. § 1.821(e), that the first-filed computer readable form filed in the '928 application be used as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date

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for the computer readable form that will be used for the instant application. A paper copy of the Sequence Listing is attached hereto and has been inserted into the specification as set forth above. Applicants have also amended the specification and claims to comply with the requirements of 37 C.F.R. § 1.821(d).

I hereby state that the content of the Sequence Listing and the computer-readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. § 1.821 (c) and (e), respectively, are the same.

I further state that the submission, filed in accordance with 37 C.F.R. § 1.821 (g) herein, does not include new matter.

If there is any fee due in connection with the filing of this Preliminary Amendment, please charge the fee to our Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

Dated: September 26, 2000

By: _____
Timothy Donaldson
Reg. No. 43,592

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NUCLEOTIDE SEQUENCES DERIVED FROM THE GENOME OF RETROVIRUSES OF THE HIV-1, HIV-2 AND SIV TYPE, AND THEIR USES IN PARTICULAR FOR THE AMPLIFICATION OF THE GENOMES OF THESE RETROVIRUSES AND FOR THE IN VITRO DIAGNOSIS OF THE DISEASES DUE TO THESE VIRUSES.

The present invention relates to oligonucleotide sequences which can be used for the implementation of techniques for the amplification of specific nucleotide sequences of human immunodeficiency retroviruses of the HIV type or of monkey immunodeficiency retroviruses of the SIV type.

The invention relates in particular to the use of such sequences for methods of in vitro diagnosis in man of the infection of an individual by a retrovirus of the HIV type (at present HIV-1 and/or HIV-2).

The isolation and characterization of retroviruses grouped together under the designations HIV-1 and HIV-2 were described in the European patent applications No. 85/905.513.9 and No. 87/400.151.4, respectively. These retroviruses were isolated from several patients exhibiting symptoms of a lymphadenopathy or an Acquired Immunodeficiency Syndrome (AIDS).

The retroviruses of the HIV-2 type like the retroviruses of the HIV-1 type are characterized by a tropism for the human T4 lymphocytes and by a cytopathogenic effect with regard to these lymphocytes when they multiply within them to give rise to, among other things, generalized and persistent polyadenopathies, or an AIDS.

Another retrovirus, designated SIV-1, this designation replacing the earlier one STLV-III, was isolated from the rhesus macaque monkey (M.D. DANIEL et al. Science, 228, 1201 (1985); N.L. LETWIN et al., Science, 230, 71 (1985) under the designation "STLV-IIImac").

Another retrovirus, designated "STLV-III_{AGM}" (or SIV_{AGM}), was isolated from wild green monkeys. However, in contrast to the viruses present in the rhesus macaque monkey, the presence of STLV-III_{AGM} does not appear to induce a disease of the AIDS type in the African green monkey.

For reasons of semantics, these viruses will be designated

in what follows only by the expression SIV (the expression SIV is an English abbreviation for "Simian Immunodeficiency Virus", possibly followed by an abbreviation designating the species of monkey from which they are derived, for example "MAC" for "macaque" or "AGM" for the "African Green Monkey".

A strain of the retrovirus SIV-1Mac was deposited with the C.N.C.M. on 7 February 1986 under the No. I-521.

The continuation of the study of the retroviruses HIV-1 and HIV-2 has also led to the production of DNA sequences (cDNA) complementary to the RNAs of their genome. The complete nucleotide sequence of a cDNA of a retrovirus representative of the HIV-2 class (HIV-2 ROD) was deposited on 21/02/1986 with the C.N.C.M. under the No. I-522, under the reference name LAV-2 ROD.

Similarly, the complete nucleotide sequence of a cDNA of a retrovirus representative of the HIV-1 class is described by WAIN-HOBSON, SONIGO, COLE, DANOS and ALIZON in CE11 (January 1985).

Also for semantic reasons, the viruses of the HIV-1 and HIV-2 type will sometimes be designated in the subsequent description by the expression HIV.

The methods for the <u>in vitro</u> diagnosis of the infections by viruses of the HIV-1 or HIV-2 type currently practised, are based on the detection of anti-HIV-1 or anti-HIV-2 antibodies possibly present in a biological sample (biopsy) or in a biological fluid, for example in a serum obtained from the patient under study, by placing this biological fluid in contact with extracts or antigens of HIV-1 or HIV-2 under conditions which could give rise to the production of an immunological reaction between these extracts or antigens and these antibodies.

There is the risk that such diagnostic methods will give rise to false negatives, in particular in the case of a recent infection of an individual by the viruses of the HIV type.

The techniques of gene amplification make a considerable contribution to the development of <u>in vitro</u> diagnostic methods which are particularly sensitive for viral diseases. Among these techniques of gene amplification, mention may be made of the PCR (Polymerase Chain

Reaction) technique as described in the European patent applications No. 86/302.298.4 of 27/03/1986 and No. 87/300.203.4 of 09/01/1987, or also the technique known as "Qßreplicase" described in Biotechnology, vol. 6 page 1197 (October 1988) and that which makes use of a RNA polymerase (T7RNA polymerase) described in the International patent application No. WO89/01050. These techniques make it possible to improve the sensitivity of detection of the nucleic acids of the virus, and require the use of specific primers for synthesis.

In the case of research on the viruses of the HIV type, the choice of primers is problematical. In fact, owing to the great variability of the nucleotide sequences of the viral genome, a primer corresponding to the known sequence of a given isolate of a virus of the HIV type may fail in the amplification of certain viral variants of the HIV type. Furthermore, even if a primer is selected from a region of the genome which is conserved from one HIV virus to another, its "efficiency" is not thereby insured and may give rise to poor amplification yields.

The precise objective of the present invention is to provide oligonucleotide primers which, inter alia, make possible the amplification of the genome of all viruses of the HIV and SIV types, in particular for diagnostic purposes, with yields considered to be maximal in the present state of the art and which, in particular, do not give rise to the presence of many aspecific bands.

The primers of the present invention are specific both for the viruses of the HIV-1 groups and/or the viruses of the HIV-2 and SIV groups, and are insensitive to variations of the genome of these viruses.

The object of the present invention is oligonucleotide primers of about 15 to 30 nucleotides which can be used for the genomic amplification of the viruses of the HIV-I type and/or HIV-2 and SIV types.

The invention relates to any nucleotide sequence characterized in that its sequence:

- is either selected from those which are contained in one of the nucleotide sequences included in the gag, vpr and pol genes of the

viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV MAC, or in the nef2, vif2 and vpx genes of the viruses HIV-2 ROD and SIV MAC, or in the env, nef1, vif1 and vpr genes of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, and more particularly from those which are contained in the nucleotide sequences defined hereafter,

- or (particularly in the case of the longest sequences) contains one of the above-mentioned nucleotide sequences derived from HIV-1 Bru or HIV-1 Mal, or HIV-1 Eli or HIV-2 ROD or SIVMac, or contains a complementary nucleotide sequence of one of these latter sequences, it being understood that the possible additional nucleotides which "extend beyond" the nucleotide sequence of the type in question at the 3' or 5' ends preferably coincide with those which are placed external to the 5' or 3' end of the same sequence within the complete sequence of the viruses of the HIV-1, HIV-2 or SIV MAC type mentioned above,

- or, if this nucleotide sequence is not identical with one of the above-mentioned nucleotide sequences, or is not complementary to one of these sequences, it is nonetheless capable of hybridizing with a nucleotide sequence derived from the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli and/or with a nucleotide sequence derived from the viruses HIV-2 ROD or SIV MAC mentioned above. The hybridization may be carried out at a temperature of 60°C $\pm$ 1°C (preferably 60°C $\pm$ 0.5°C), recommended for an optimal yield.

The numbering of the nucleotides mentioned below corresponds to that used in the reference manual "Human Retrovirus and AIDS-1989" edited by the "Los Alamos National Laboratory - New Mexico - USA".

(The sequences of the viruses HIV-1 Mal, HIV-1 Eli were described by MONTAGNIER, SONIGO, WAIN-HOBSON and ALIZON in the European patent application No. 86.401380 of 23/06/86).

The sequences of the invention are synthesized in a synthesizer marketed by Applied Biosystems (phosphoro-amidite method) or in any other apparatus employing a similar method.

The invention relates more particularly to the oligonucleotide sequences characterized by the following nucleotide sequences (shown in the 5'$\longrightarrow$3' sense; the initials "S" and "AS" indicate whether the

oligonucleotide is sense or anti-sense, i.e. whether the oligonucleotide is oriented in the 5' ⟶ 3' or in the 3' ⟶ 5' sense):

1°) sequences common to the genomes of the HIV-1, HIV-2 and SIV viruses (the pairs of numbers separated by a dash indicate the position of the nucleotides in the genomes corresponding respectively to the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV):

. specific sequences of the gag gene of the genome of the above-mentioned viruses (gene coding for a group of antigens specific for the nucleoid of these viruses).

Certain variants may be introduced by certain positions of the nucleotide sequences indicated below, without affecting the hybridization properties of these nucleotide sequences with the genes of the viruses of the HIV and/or SIV types. The nucleotide sequences containing these variants are shown below the original nucleotide sequences from which they are derived by substitution of one or more bases. The bases representing modifications of the initial nucleotide sequences are indicated by a letter directly beneath the base which they replace in the initial sequences; whereas the bases of the original sequences which are not replaced in the sequences bearing these variants are shown by dots.

The synthesis of the primers is carried out by using all of the variants simultaneously. It is the mixture of all of the variants for a given sequence which is used in the tests.

MMy1 : TGG CGC CCG AAC AGG GAC
... ... .T. ... ...
S, 636-653, 635-652, 636-653, 859-876, 834-851

MMy2 : GGC CAG GGG GAA AGA AAA A
... .C. .C. ... ...
... ... .A. ... ...
S,854-872,864-888,848-872,1160-1184, 1124-1148

MMy3 : TGC CCA TAC AAA ATG TTT TA
... ... C.. T.T ... .
AS,900-881,916-897,900-881,1212-1193,1176-1157

MMy4 : TGC ATG GCT GCT TGA TG
... ..A ... ..C ..G ..
AS,1385-1369,1419-1403,1385-1369,1703-1687,1667-1651

MMy4B : CTT TGC ATG GCT GCT TGA TG
..C ... ..A ... ..C ..G ..
AS, 1388-1369, 1421-1403, 1388-1369, 1706-1687,
1670-1651,

MMy4Ba : CAT CAA GCA GCC ATG CAA AG
..C ..G ... ..T ... ..G ..
S, 1369-1388, 1403-1421, 1369-1388,
1687-1706, 1651-1670,

MMy28 : AGG GCT GTT GGA AAT GTG G
... ...G ... .
S, 2021-2039, 2055-2073, 2024-2042, 2329-2349,
2299-2318,

MMy28a : CCA CAT TTC CAG CAT CCC T
... ...G ... .
... ...C ... .
AS, 2039-2021, 2073-2055, 2042-2024, 2349-2329,
2318-2299

- specific sequences of the vpr gene :

MMy18 : GAT AGA TGG AAC AAG CCC CAG
S, 5590-5610, 5585-5605, 5554-5574, 6233-6296,
6147-6170,

MMy19 : TCC ATT TCT TGC TCT CCT CTG T
AS, 5870-5849, 5865-5844, 5834-5813,
6551-6531, 6454-6431,

· specific sequences of the pol gene :

MMy29 : TAA AGC CAG GAA TGG ATG GCC CAA
... ... .A. ...
S, 2620-2643, 2615-2638, 2584-2607, 2971-2994,
2887-3010

MMy29a : TTG GGC CAT CCA TTC CTG GCT TTA
... .T. ... ...
AS, 2643-2620, 2638-2615, 2607-2584, 2994-2971,
3010-2887,

MMy30 : TGG ACT GTC AAT GAC ATA CAG AA
... ...T ... .
S, 3339-3361, 3334-3356, 3303-3325, 3690-3712,
3606-3628,

MMy30a : TTC TGT ATG TCA TTG ACA GTC CA
... ...T ... ..
AS, 3361-3339, 3356-3334, 3325-3303, 3712-3690,
3628-3606,

MMy31 : CAT GGG TAC CAG CAC ACA AAG G
S, 4186-4207, 4181-4202, 4150-4171, 4534-4555,
4450-4471,

MMy31a : CCT TTG TGT GCT GGT ACC CAT G
AS, 4207-4186, 4202-4181, 4171-4150, 4555-4534,
4471-4450,

MMy32 : TGG AAA GGT GAA GGG GCA GT
... ...A ... ..
S, 4992-5011, 4987-5006, 4956-4975, 5340-5359,
5256-5275,

MMy32 : ACT GCC CCT TCA CCT TTC CA
... ...T ... .
... ...C ... .
AS, 5011-4992, 5006-4987, 4975-4956, 5359-5340,
5275-5256

2°) sequences common to the genomes of the HIV-2 and SIV viruses (the pairs of numbers separated by a dash indicate the position of the nucleotides in the genomes corresponding to the viruses HIV-2 ROD and SIV-MAC, respectively).

. specific sequences of the nef2 gene (coding for a negative factor of 27 kD)

MMy12 : AGA GAC TCT TGC GGG CGC GTG
S, 9165-9185, 9139-9159,

MMy13 : ATA TAC TTA GAA AAG GAA GAA GG
S, 9542-9564, 9516-9538,

MMy13bis : CCT TCT TCC TTT TCT AAG TAT AT
AS, 9564-9542, 9538-9516,

MMy14 : AGC TGA GAC AGC AGG GAC TTT CCA
AS, 9956-9933, 9893-9870,

. specific sequences of the vif2 gene (coding for an infectivity factor of 23 kD)

MMy20 : TAT GGA GGA GGA AAA GAG ATG GAT AGT
S, 5424-5450, 5340-5366,

MMy21 : TAG CAC TTA TTT CCC TTG CTT T
S, 5754-5775, 5670-5691,

MMy21bis : AAA GCA AGG GAA ATA AGT GCT A
AS, 5775-5754, 5691-5670,

MMy22 : CCC TTG TTC ATC ATG CCA GTA T
AS, 6082-6061, 5995-5974,

. specific sequences of the vpx gene (coding for a protein of 12 kD)

MMy23 : ATG TCA GAT CCC AGG GAG A
S, 5900-5918, 5813-5831,

MMy24 : CCT GGA GGG GGA GGA GGA GGA
AS, 6228-6208, 6141-6121,

3°) Sequences common to the genomes of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli (the pairs of numbers separated by a dash indicate the position of the nucleotides in the genomes corresponding to the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, respectively).

. specific sequences of the env gene (coding for the envelope proteins)

MMy5 : CCA ATT CCC ATA CAT TAT TGT GCC CC
S,6905-6930,6903-6928,6860-6885
MMy5 : GGG GCA CAA TAA TGT ATG GGA ATT GG
AS, 6930-6905, 6928-6903, 6885-6860,
MMy6 : AAT GGC AGT CTA GCA GAA GAA GA
S,7055-7077,7053-7075,7010-7032
MMy7 : ATC CTC AGG AGG GGA CCC AGA AAT T
S, 7360-7384, 7349-7373,7306-7330
MMy7 a : AAT TTC TGG GTC CCC TCC TGA GGA T
AS, 7384-7360,7373-7349,7330-7306
MMy8 : GTG CTT CCT GCT GCT CCC AAG AAC CC
AS, 7857-7832,7846-7821,7800-7775
MMy8.a : GGG TTC TTG GGA GCA GCA GGA AGC AC
S, 7832-7857, 7821-7846, 7775-7800,
MMy9 : ATG GGT GGC AAG TGG TCA AAA AGT AG
... ...A ... ...
S,8844-8869, 8836-8861, 8787-8812,
MMy9 a : CTA CTT TTT GAC CAC TTG CCA CCC AT
AS, 8869-8844, 8861-8836, 8812-8787,
MMy78 : TAT TAA CAA GAG ATG GTG G
S, 7629-7647, 7612-7630, 7572-7590,
MMy89 : CCA GCA AGA AAA GAA TGA A
S, 8224-8242, 8213-8231, 8167-8185,
MMy89 a : TTC ATT CTT TTC TTG CTG G
AS, 8242-8224, 8231-8213, 8185-8167,

. specific sequences of the nef 1 gene :

MMy10 : AAA AGA AAA GGG GGG ACT GGA
S, 9116-9136, 9117-9137, 9062-9082,
MMy10a : TCC AGT CCC CCC TTT TCT TTT
AS,9136-9116, 9137-9117, 9082-9062,

MMy11 : AAA GTC CCC AGC GGA AAG TCC C
AS,9503-9483, 9505-9484, 9449-9428,

specific sequences of the vif 1 gene

MMy15 : GAT TAT GGA AAA CAG ATG GCA GGT GAT
S, 5073-5099, 5068-5094, 5037-5063,
MMy16 : GCA GAC CAA CTA ATT CAT CTG TA
S, 5383-5405, 5378-5400, 5347-5369,
MMy16a : TAC AGA TGA ATT AGT TGG TCT GC
AS, 5405-5383, 5400-5378, 5369-5347,
MMy17 : CTT AAG CTC CTC TAA AAG CTC TA
AS, 5675-5653, 5670-5648, 5639-5617,

specific sequences of the vpu gene

MMy25 : GTA AGT AGT ACA TGT AAT GCA ACC T
S, 6081-6105, 6076-6100, 6045-6069,
MMy26 : AGC AGA AGA CAG TGG CCA TGA GAG
S, 6240-6263, 6238-6261, 6207-6230,
MMy27 : ACT ACA GAT CAT CAA TAT CCC AA
AS, 6343-6321, 6338-6316, 6307-6285,

The object of the invention is also the sequences (or primers) possessing a complementary nucleotide structure to those of the primers defined above.

It also relates to the nucleotide sequences possessing certain mutations with respect to those defined above without the hybridization properties, such as defined above, of these sequences being modified. The percentage of nucleotides different from those constituting the sequences described above without thereby affecting the hybridization properties of the sequences of the invention may attain 40%.

Generally speaking, in the case of a sense (S) primer, a larger number of mutations is tolerated at the 5' end than at the 3' end of the primer, the 3' end being required to hybridize perfectly with a specific strand of a nucleotide sequence in order for this sequence to be amplified. In the case of an anti-sense (AS) primer, it is at the 3' end that tolerance is allowed.

The object of the invention is also the primers such as those defined above and including a conserved stretch of at least 5 bases on either side of the central part which contains modifications without the above hybridization properties being modified.

One of the characteristics of the oligonucleotide primers of the invention is that of giving a clear-cut amplification band, usually free of aspecific bands when the technical directions for use described in the present invention are followed. This fact is due to the length of the primers which may attain 27 bases and thus increases the specificity of hybridization, as well as to the drastic conditions of use which make it possible to eliminate parasitic combinations. In addition to the percentage of homology with the reference matrix, the specificity for each type of virus is a function of the length of the primer which may attain as many as 40 bases in order to obtain an acceptable yield.

The invention also includes primers such as those described above linked at their 5' end to a promoter for the implementation of a method of genomic amplification by the synthesis of multiple copies of DNA or RNA such as that described in the European patent application No. 88/307.102.9 of 01/08/1988.

The object of the invention is in particular the use of the primers described above for the implementation of a procedure of gene amplification of nucleotide sequences of the viruses of the HIV-1 and/or HIV-2 and/or SIV type, this procedure being applicable to the <u>in vitro</u> diagnosis of the potential infection of an individual by a virus of the HIV-1 and/or HIV-2 type or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV).

This method of <u>in vitro</u> diagnosis of the invention is carried out starting from a biological sample (for example a biological fluid

such as serum, the lymphocytes of circulating blood) obtained from a patient under study, and comprising mainly the following steps:

- a step involving the extraction of the nucleic acid to be detected belonging to the genome of the virus of the HIV-1 and/or HIV-2 and/or SIV type possibly present in the above-mentioned biological sample and, where appropriate, a step involving the incubation of the said nucleic acid with a reverse transcriptase if this latter is in the form of RNA in order to obtain a double-stranded nucleic acid (this last step being also designated below as the step of retrotranscription of the viral RNA),
- a cycle comprising the following steps:
  - . denaturation of the double-stranded nucleic acid to be detected, which leads to the formation of a single stranded nucleic acid,
  - . hybridization of each of the strands of the nucleic acid obtained during the previous denaturation step with at least one primer according to the invention, by placing the strands mentioned above with at least one primer couple according to the invention under the conditions of hybridization defined below,
  - . formation, starting from the primers, of the DNA complementary to the strands to which they are hybridized in the presence of a polymerization agent (DNA polymerase) and the four different nucleoside triphosphates (dNTP) which leads to the formation of a greater number of double-stranded nucleic acids to be detected than in the previous denaturation step, this cycle being repeated a defined number of times in order to obtain the said nucleic acid sequence to be detected possibly present in the biological sample in an amount sufficient to allow its detection,
- a step involving the detection of the possible presence of the nucleic acid belonging to the genome of the virus of the HIV-1 and/or HIV-2 and/or SIV type in the biological sample.

The hybridization step described above is advantageously performed at 60°C for 1 minute 30 seconds in the "10 X buffer", the composition of which (expressed as final concentrations for use) is indicated below.

The method of in vitro diagnosis of the invention may be carried out either starting from the viral RNA, or from the episomal or integrated complementary DNA.

In fact, the genomes of the HIV and SIV viruses exist in the form of RNA or DNA, depending on the localization of the virus in the organism.

When the virus is situated within the cells of the organism, in particular in the interior of blood cells, its RNA is recopied into DNA by a reverse transcriptase. On the other hand, the genome of the viruses of the HIV type in the extracellular medium, in particular in the blood, remains in the RNA form.

The extraction step according to the invention of the viral DNA contained in the cells of the biological sample recommended by the inventors - in addition to the standard method using phenol/chloroform - comprises the following steps:

. suspension of the cell pellet in 0.5 ml of boiled water in a Potter homogenizer with a wide pestle,

. grinding of the cells by "forwards and backwards rotation",

. addition of Triton X100 to give a final concentration of 0.1%,

. heat denaturation for 15 to 25 minutes at 100°C,

. brief centrifugation in order to remove only the cell debris,

. precipitation of the DNA overnight at -20°C by addition of 2.5 volumes of absolute ethanol and 10% of the final volume of 3 molar sodium acetate. The DNA is subsequently recovered, then resuspended in boiled water after having been washed twice with 70° ethanol. It should be noted that this method leads to the simultaneous precipitation of the DNAs and the RNAs which make possible the detection of the genomic message of the viruses of the HIV or SIV types by use of the method called "direct PCR-DNA" or by that called "PCR-RNA".

The step involving the extraction of the viral RNA is usually performed in the classical manner well-known to the person skilled in the art.

After extraction of the RNA, it is necessary to carry out an additional step involving the transformation of the single-stranded RNA into double-stranded DNA when the in vitro diagnosis of the

invention is performed on biological samples containing the viruses of the HIV-1 and/or HIV-2 and/or SIV types, the genomes of which are in the RNA form.

This transformation of the RNA into DNA is carried out by treatment of the RNA obtained after extraction of the biological sample, in particular serum, with a reverse transcriptase in a suitable medium.

The object of the invention more particularly among other things is a method of in vitro diagnosis such as that defined above in which the step of retrotranscription of viral RNA is carried out in the following manner:

- 10 µg of RNA, extracted and resuspended in water, is placed in the presence of the primer couple at a concentration of 40 µM of each in a final volume of 40 µl. The mixture is denatured at 100°C for 10 minutes, then plunged into ice-cold water,
- 10 µl of the following mixture are added: 5 µl of the "10 X buffer" described below + 1 unit of AMV (Avian Myeloblastosis Virus) or MuMLV (Moloney Leukemia Virus) reverse transcriptase + 1 unit of Taq-polymerase + 1 µl of a 25 mM mixture of each of the 4 dNTP + water as required to give 10 µl. The final volume is thus 50 µl.

This reaction is carried out in two steps:

- a) 1st step: synthesis of the cDNA by the action of the reverse transcriptase at 42°C for 13 minutes,

- b) 2nd step: standard gene amplification: the mixture is heated at 95°C for 3 minutes to destroy the reverse transcriptase and to carry out the dehybridization/hybridization step, then the cycle previously described for gene amplification is initiated.

The object of the invention is more particularly a method of in vitro diagnosis such as that described above in which the denaturation step is performed in the presence of one or several primer couples of the invention. In fact, as has been specified above, one of the characteristics of the oligonucleotides (or primers) of the invention is that they give a clear-cut amplification band, usually free of aspecific bands, when they are used under the following conditions:

- hybridization: the primers (1 µl of a 40 µmolar (40 µM) solution

of each primer) are placed in the presence of the matrix DNA (100 to 300 ng) for the first step of denaturation-reassociation; the tubes containing this mixture of matrix DNA and primers is heated for 10 minutes at 100°C, then plunged into ice-cold water in order to increase the extent of matrix DNA/primer reassociation. The primers must be used at a final concentration of 0.8 µM each in the amplification step which follows.

- amplification: the 4 dNTPs are added to the preceding mixture, each being used at a concentration of 0.5 µmolar in the final solution (50 µl), and one unit of Taq-polymerase per 50 µl of reaction mixture; this step is carried out in an amplification buffer of the present invention, usually designated by the name "10 X buffer", the composition of which (when it is diluted 1/10) is the following: Tris-HCl, pH 8.9: 50 mM; $(NH_4)_2SO_4$: 15 mM; $MgCl_2$: 5 mM; ß-mercaptoethanol: 10 mM; gelatin: 0.25 mg/ml. 5 µl of this buffer and water to give 50 µl are added to the preceding mixture.

The amplification cycles are performed in the following manner: 30 to 40 cycles consisting of:

. 94°C for 10 seconds (denaturation),

. 60°C for 1 minute 30 (hybridization),

. 78°C for 1 minute 30 (elongation).

The whole series is followed by a single cycle at 78°C for 15 minutes.

The accuracy to ± 0.3°C of the temperatures indicated as well as their stability during the different parts of the cycles, are essential conditions for the production of maximal yields as well as insuring the absence of aspecific bands.

The optimal concentration of DNA is 100 to 300 ng in the case of genomic DNA extracted from cells (of patients or in culture, mammals or other species).

It is obvious that the preceding conditions represent optimal conditions for a final reaction mixture of 50 µl, and that these conditions may be modified, depending on the final volume of the reaction mixture.

The use of several different primer couples (or cocktails

of couples) of the invention makes possible either the cross-detection of several types of the viruses of the HIV and/or SIV type, or the simultaneous detection of several genes of a given virus of the HIV and/or SIV type.

As examples of the preferred primer couples which can be used within the framework of the present invention, mention may be made of the following primer couples:

- MMy1-MMy4, MMy2-MMy4, MMy1-MMy3, MMy18-MMy19, MMy4a-MMy28a, MMy28-MMy29a, MMy29-MMy30a, MMy31-MMy32a, in particular for the in vitro diagnosis of the infection of an individual by HIV-1 and/or HIV-2
- MMy5-MMy8, MMy6-MMy8, MMy7-MMy8, MMy5-MMy7a, MMy6-MMy7a, MMy9-MMy11, MMy10-MMy11, MMy9-MMy10a, MMy26-MMy5a, MMy8a-MMy9a, MMy8a-MMy89, MMy89a-MMy9a, MMy15-MMy17, MMy15-MMy16a, MMy16-MMy17, MMy25-MMy27, MMy26-MMy27, in particular for the in vitro diagnosis of the infection of an individual by HIV-1,
- MMy20-MMy22, MMy20-MMy21a, MMy21-MMy22, MMy23-MMY24, MMy12-MMy14, MMy12-MMy13a, for the in vitro diagnosis of the infection of an individual by HIV-2.

The agent of polymerization used in the elongation step of the cycle is a thermostable DNA polymerase, in particular Taq polymerase, the amplifiose of the Appligene company or any thermostable DNA polymerase which is commercially available.

Generally speaking, the cycle of the method of in vitro diagnosis of the invention is repeated between 30 and 40 times.

Depending on the nucleotide primer couples used, the method of in vitro diagnosis of the invention also makes it possible to detect selectively the genes of the viruses of the HIV and/or SIV type present in the biological sample.

As examples of the primer couples which can be used for the above-mentioned method of diagnosis gene-per-gene of the invention are the following:

- MMy1-MMy4, MMy2-MMy4, MMy1-MMy3, MMy4a-MMy28a for the gag gene,
- MMy18-MMy19 for the vpr gene,
- MMy5-MMy8, MMy6-MMy8, MMy7-MMy8, MMy5-MMy7a, MMy6-MMy7a, MMy26-MMy5a, MMy8a-MMy9a, MMy8a-MMy89, MMy89a-MMy9a for the env gene,

- MMy9-MMy11, MMy9-MMy10a, MMy10-MMy11 for the nef1 gene,
- MMy15-MMy17, MMy15-MMy16a, MMy16-MMy17 for the vif1 gene,
- MMy20-MMy22, MMy20-MMy21a, MMy21-MMy22 for the vif 2 gene,
- MMy23-MMy24 for the vpx gene,
- MMy12-MMy14, MMy12-MMy13a, MMy13-MMy14 for the nef2 gene,
- MMy25-MMy27, MMy26-MMy27 for the vpu gene,
- MMy28-MMy29a, MMy29-MMy30a, MMy30-MMy31a, MMy31-MMy32a for the pol gene.

However, the combinations between "S" and "AS" primers described above are not limiting and may be varied according to the wish of the user.

The sizes of the nucleotide fragments synthesized with the aid of the primer couples mentioned above as examples are shown in the following Tables I to XI:
(the figures indicated in the Tables below represent the number of nucleotides in the fragments synthesized, and the "dashes" indicate that the primer couples tested do not make it possible to characterize the corresponding viral strains).

Table I

	gag		gag	
	MMy1-MMy3	MMy1-MMy4	MMy2-MMy4	MMy4a -MMy28a
HIV1-BRU:	265	750	532	671
HIV1-MAL:	282	785	556	671
HIV1-ELI:	265	750	538	674
HIV2-ROD:	354	845	544	663
SIV :	343	844	544	668

Table II

	env		env	
	MMy5-MMy7a	MMy5-MMy8	MMy6-MMy7a	MMy6-MMy8
HIV1-BRU:	480	953	330	803
HIV1-MAL:	471	944	321	794
HIV1-ELI:	471	941	321	791
HIV2-ROD:	-	-	-	-
SIV :	-	-	-	-

Table III

	env		env
	MMy7-MMy8	MMy26-MMy5.a	MMy8 a -MMy9 a
HIV1-BRU:	498	691	1038
HIV1-MAL:	498	691	1041
HIV1-ELI:	495	679	1038
HIV2-ROD:	-	-	-
SIV :	-	-	-

Table IV

	env	env
	MMy8 a -MMy89	MMy89 a -MMy9 a
HIV1-BRU:	411	646
HIV1-MAL:	411	649
HIV1-ELI:	411	646
HIV2-ROD:	-	-
SIV :	-	-

Table V

	nef1	nef1	
	MMy9-MMy10 a	MMy9-MMy11	MMy10-MMy11
HIV1-BRU:	293	660	388
HIV1-MAL:	302	660	388
HIV1-ELI:	296	663	388
HIV2-ROD:	-	-	-
SIV :	-	-	-

Table VI

	nef2		nef2
	MMy12-MMy13a	MMy12-MMy14	MMy13-MMy14
HIV1-BRU:	-	-	-
HIV1-MAL:	-	-	-
HIV1-ELI:	-	-	-
HIV2-ROD:	400	792	415
SIV :	400	755	378

Table VII

	vif1		vif1
	MMy15-MMy16a	MMy15-MMy17	MMy16-MMy17
HIV1-BRU:	333	603	293
HIV1-MAL:	333	603	293
HIV1-ELI:	333	603	293
HIV2-ROD:	-	-	-
SIV :	-	-	-

Table VIII

	vpr	vif2	
	MMy18-MMy19	MMy20-MMy21a	MMy20-MMy22
HIV1-BRU:	281	-	-
HIV1-MAL:	281	-	-
HIV1-ELI:	281	-	-
HIV2-ROD:	319	352	659
SIV :	308	352	656

Table IX

	vif2	vpx
	MMy21-MMy22	MMy23-MMy24
HIV1-BRU:	-	-
HIV1-MAL:	-	-
HIV1-ELI:	-	-
HIV2-ROD:	329	329
SIV :	326	329

Table X

	vpu		pol	
	MMy25-MMy27	MMy26-MMy27	MMy28-MMy29a	
HIV1-BRU:	263	104	623	
HIV1-MAL:	263	101	584	
HIV1-ELI:	263	101	584	
HIV2-ROD:	-	-	666	
SIV :	-	-	712	

Table XI

	pol		pol	
	MMy29-MMy30a	MMy30-MMy31a	MMy31-MMy32a	
HIV1-BRU:	742	869	826	
HIV1-MAL:	742	869	826	
HIV1-ELI:	742	869	826	
HIV2-ROD:	742	866	826	
SIV :	742	866	826	

It is to be noted that owing to their arrangement on the genome, the primers used for amplification may be combined in a manner such that they can be used as probes, either after labelling with ^{32}P by means of a kinase, or for use in the procedure employing cold probes to check the specificity of the amplification band observed during an analysis by "Southern blot". In addition to the classical combination of the primers in order that a third oligonucleotide may serve as specific internal probe, the special case of the vif1/vpr and vif2/vpx genes due to the overlapping of these genes, which permits cross-detection, is to be noted. Furthermore, during an analysis of the amplified DNA by sequencing, these oligonucleotides may be used as specific primers for the DNA polymerase making possible a duplicate sequencing in each sense, hence a duplicate reading of the sequences, thus removing possible ambiguities in interpretation.

The object of the invention is also the primers such as those defined above, labelled in particular radioactively or enzymatically, as well as their use as nucleotide probes, in particular in the framework of the method of in vitro diagnosis such as described above.

The object of the invention is also oligonucleotides such as those described above and containing sugars in the α-conformation. Such oligonucleotides exhibit the property of reversing the sense of the double helix formed with the matrix (strand of the genome of the virus), this double helix thus passing from the "S" state to the "AS" state.

The invention also relates to the oligonucleotides described above in which some nucleotides are methylated and/or contain one or more sulfur atoms, in particular at the adenine residues. Such oligonucleotides possess the property of increasing the stability of the double helix and consequently of hybridizing better with the DNA strand to be amplified.

The invention also relates to the oligonuceotides such as those described above existing in the so-called "modified base" form containing nucleotides to which chromophores are covalently grafted (planar aromatic molecules such as acridine orange), in particular according to the method described in the article by C. Hélène published

in "la Vie des Sciences", compte-rendus, série générale, tome 4, No. 1, p. 17-37. Such oligonucleotides possess the property of being easily detectable, in particular by fluorescence.

The oligonucleotides of the invention can also be used for the implementation of a method of in vitro diagnosis of the infection of monkeys (macaque, mangabey monkey or green monkey) by the virus of the SIV type, this method duplicating the principal characteristics of that described above.

The object of the invention is also diagnostic kits for the implementation of the methods of in vitro diagnosis mentioned above. As an example, a diagnostic kit of the present invention contains:

- at least one oligonucleotide primer couple according to the invention, each couple consisting of a primer which hybridizes with one of the strands of the nucleic acid sequence to be detected, and a primer which hybridizes with the complementary strand of this latter under the conditions defined above,
- suitable reagents for the implementation of the cycle of amplification operations, in particular a DNA polymerase and the four different nucleoside triphosphates, and the reaction medium designated "10 x buffer" described above.
- one (or more) probe which can be labelled, in particular by radioactivity, and which is capable of hybridizing specifically in the labelled or unlabelled form with the amplified nucleic acid sequence(s) to be detected.

The invention also relates to the use of the primers of the invention indicated above for the implementation of a procedure for the synthesis of proteins encoded in the nucleotide sequences amplified by means of these primers.

As an illustration, this procedure for the synthesis of proteins comprises the amplification of the nucleotide sequences of the genomes of the viruses of the HIV or SIV type (coding for a specific protein and, where appropriate, having undergone certain modifications of their nucleotides) by placing in contact the said sequences with at least one primer couple according to the invention under the conditions described above, followed by the translation of these

sequences thus amplified into proteins; this last step is carried out in particular by transformation of suitable host cells with the aid of vectors containing the said amplified sequences, and the recovery of the proteins produced in these host cells.

The invention also relates to the polypeptides derived from the translation of the nucleotide sequences (or primers) of the invention.

The object of the invention is also the use of the anti-sense oligonucleotide primers as antiviral agents in general, in particular to combat AIDS, as well as pharmaceutical compositions containing these anti-sense primers in combination with a pharmaceutically acceptable vehicle.

The invention also relates to the immunogenic compositions containing one or more translation products of the nucleotide sequences according to the invention, and/or one or more translation products of the nucleotide sequences amplified according to the procedures described above starting from primers defined according to the invention, these translation products being combined with a pharmaceutically acceptable vehicle.

The invention relates to the antibodies directed against one or more of the translation products described above (or, in other terms, capable of giving rise to an immunological reaction with one or more translation products of the nucleotide sequences according to the invention, or also one or more translation products of the amplified nucleotide sequences starting from primers defined according to the invention) and their use for the implementation of methods of in vitro diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type, or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV) according to the procedures well-known to the person skilled in the art.

As an illustration, such a method of in vitro diagnosis according to the invention comprises the placing in contact of a biological sample (in particular serum), taken from a patient under study, with antibodies according to the invention, and the detection by means of any appropriate procedure (in particular with the aid of

labelled anti-immunoglobulins) of the immunological complexes formed between the antigens of the viruses of the HIV or SIV type possibly present in the biological sample and the said antibodies.

The object of the invention is also kits for in vitro diagnosis containing antibodies according to the invention and, where appropriate, suitable reagents for the detection of the immunological complex formed by reaction between the said antibodies and the antigens of the HIV or SIV viruses.

The invention also relates to a procedure for the preparation of the polypeptides mentioned above, in particular those corresponding according to the universal genetic code to the nucleotide sequences (or primers) described above, this procedure being characterized in that, starting preferably from the C-terminal amino acid, successive amino acid residues are condensed successively one at a time in the required order, or amino acid residues and fragments previously formed and already containing several amino acid residues in the required order are condensed, or also several fragments thus prepared beforehand are condensed, it being understood that care will be taken to protect beforehand all of the reactive functions borne by these amino acid residues or fragments with the exception of the amine function of the one and the carboxyl function of the other, which normally must participate in the formation of the peptide bonds, in particular after activation of the carboxyl function according to the known methods of peptide synthesis and this is continued in a stepwise manner until the N-terminal amino acid is reached.

For example, recourse may be had to the procedure of peptide synthesis in homogeneous solution described by Houbenweyl in "Methoden der Organischen Chemie" (Methods of Organic Chemistry) edited by W. Wunsch, vol. 15-I and II, THIEME, STUTTGART, 1974, or to that of peptide synthesis on a solid phase described by R.D. Merrifield in "Solid Phase Peptide Synthesis" (J. Am. Chem. Soc., 45, 2149-2154).

The invention also relates to a procedure for the preparation of the nucleotide sequences (or primers) described above, this procedure comprising the following steps:

- incubation of the genomic DNA, isolated from one of the viruses of

the HIV or SIV type mentioned above, with DNAase I, then addition of EDTA and purification by extraction with the mixture phenol/chloroform/isoamyl alcohol (25/24/1), then by ether,

- treatment of the DNA thus extracted by Eco R1 methylase in the presence of DTT, and purification by extraction as described above,
- incubation of the DNA thus purified with the 4 deoxynucleoside triphosphates dATP, dCTP, dGTP and dTTP in the presence of T4 DNA polymerase and DNA ligase of E.coli, then purification according to the method described above,
- the cloning of the nucleic acid thus obtained in a suitable vector and the recovery of the desired nucleic acid with the aid of a suitable probe.

A particularly useful procedure for the preparation of the nucleotide sequences of the invention comprises the following steps:

- the synthesis of DNA by using the ß-cyanoethyl phosphoramidite automated method described in Bioorganic Chemistry 4, 274-325 (1986),
- the cloning of the nucleic acid thus obtained in a suitable vector and the recovery of the nucleic acid by hybridization with a suitable probe.

Another procedure for the preparation of the nucleotide sequences of the invention comprises the following steps:

- the set of chemically synthesized oligonucleotides, provided with various restriction sites at their ends, the sequences of which are compatible with the sequence of amino acids of the natural polypeptide according to the principle described in Proc. Natl. Acad. Sci. USA, 80, 7461-7465 (1983),
- the cloning of the nucleic acid thus obtained in a suitable vector and the recovery of the desired nucleic acid by hybridization with a suitable probe.

CLAIMS

1. Nucleotide sequence characterized in that its sequence:
- is either selected from those which are contained in one of the nucleotide sequences comprised in the gag, vpr and pol genes of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV MAC, or in the nef2, vif2 and vpx genes of the viruses HIV-2 ROD and SIV MAC, or in the env, nef1, vif1 and vpr genes of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli,
- or (particularly in the case of the longest primers) contains one of the above-mentioned nucleotide sequences derived from HIV-1 Bru or HIV-1 Mal or HIV-1 Eli or HIV-2 ROD or SIV MAC, or contains a complementary nucleotide sequence to one of these latter sequences, it being understood that the possible additional nucleotides which "extend beyond" the nucleotide sequence of the type in question at the 3' or 5' end coincide preferably with those which are placed external to the 3' or 5' end of the same sequence within the complete sequence of the viruses of the HIV-1, HIV-2 or SIV MAC type mentioned above,
- or, if the sequence of this primer is not identical with one of the above-mentioned nucleotide sequences, or is not complementary to one of these sequences, is nonetheless capable of hybridizing with a nucleotide sequence derived from the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli and/or with a nucleotide sequence derived from the HIV-2 ROD or SIV MAC viruses mentioned above.

2. Sequences according to Claim 1 contained in the gag gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

```
MMy1 :   TGG CGC CCG AAC AGG GAC
         ... ... .T. ... ... ...
      S, 636-653, 635-652, 636-653, 859-876, 834-851
MMy2 :    GGC CAG GGG GAA AGA AAA A
          ... .C. .C. ... ... ... .
          ... ... .A. ... ... ... .
      S,854-872,864-888,848-872,1160-1184, 1124-1148
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MMy3 : TGC CCA TAC AAA ATG TTT TA
... ... C.. T.T ... .
AS,900-881,916-897,900-881,1212-1193,1176-1157
MMy4 : TGC ATG GCT GCT TGA TG
... ..A ... ..C ..G ..
AS,1385-1369,1419-1403,1385-1369,1703-1687,1667-1651
MMy4B : CTT TGC ATG GCT GCT TGA TG
..C ... ..A ... ..C ... ..
AS, 1388-1369, 1421-1403, 1388-1369, 1706-1687,
1670-1651,
MMy4B.a : CAT CAA GCA GCC ATG CAA AG
..C ..G ... ..T ... ..G ..
S, 1369-1388, 1403-1421, 1369-1388,
1687-1706, 1651-1670,
MMy28 : AGG GCT GTT GGA AAT GTG G
... ... .G. ... .
S, 2021-2039, 2055-2073, 2024-2042, 2329-2349,
2299-2318,
MMy28 a : CCA CAT TTC CAG CAT CCC T
... ...G ... .
... ...C ... .
AS, 2039-2021, 2073-2055, 2042-2024, 2349-2329,
2318-2299

3. Sequences according to Claim 1 contained in the vpr gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy18 : GAT AGA TGG AAC AAG CCC CAG
S, 5590-5610, 5585-5605, 5554-5574, 6233-6296,
6147-6170,
MMy19 : TCC ATT TCT TGC TCT CCT CTG T
AS, 5870-5849, 5865-5844, 5834-5813,
6551-6531, 6454-6431,

4. Sequences according to Claim 1 contained in the pol gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy29 : TAA AGC CAG GAA TGG ATG GCC CAA
... ... .A. ...
S, 2620-2643, 2615-2638, 2584-2607, 2971-2994, 2887-3010

MMy29a : TTG GGC CAT CCA TTC CTG GCT TTA
... .T. ... ...
AS, 2643-2620, 2638-2615, 2607-2584, 2994-2971, 3010-2887,

MMy30 : TGG ACT GTC AAT GAC ATA CAG AA
... ...T ... .
S, 3339-3361, 3334-3356, 3303-3325, 3690-3712, 3606-3628,

MMy30a : TTC TGT ATG TCA TTG ACA GTC CA
... ...T ... ..
AS, 3361-3339, 3356-3334, 3325-3303, 3712-3690, 3628-3606,

MMy31 : CAT GGG TAC CAG CAC ACA AAG G
S, 4186-4207, 4181-4202, 4150-4171, 4534-4555, 4450-4471,

MMy31a : CCT TTG TGT GCT GGT ACC CAT G
AS, 4207-4186, 4202-4181, 4171-4150, 4555-4534, 4471-4450,

MMy32 : TGG AAA GGT GAA GGG GCA GT
... ...A ... ..
S, 4992-5011, 4987-5006, 4956-4975, 5340-5359, 5256-5275,

MMy32a : ACT GCC CCT TCA CCT TTC CA
... ...T ... .
... ...C ... .
AS, 5011-4992, 5006-4987, 4975-4956, 5359-5340, 5275-5256

5. Sequences according to Claim 1 contained in the nef 2 gene of the viruses HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy12 : AGA GAC TCT TGC GGG CGC GTG
S, 9165-9185, 9139-9159,

MMy13 : ATA TAC TTA GAA AAG GAA GAA GG
S, 9542-9564, 9516-9538,

MMy13a : CCT TCT TCC TTT TCT AAG TAT AT
AS, 9564-9542, 9538-9516,

MMy14 : AGC TGA GAC AGC AGG GAC TTT CCA
AS, 9956-9933, 9893-9870,

6. Sequences according to Claim 1 contained in the vif 2 gene of the viruses HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy20 : TAT GGA GGA GGA AAA GAG ATG GAT AGT
S, 5424-5450, 5340-5366,

MMy21 : TAG CAC TTA TTT CCC TTG CTT T
S, 5754-5775, 5670-5691,

MMy21a : AAA GCA AGG GAA ATA AGT GCT A
AS, 5775-5754, 5691-5670,

MMy22 : CCC TTG TTC ATC ATG CCA GTA T
AS, 6082-6061, 5995-5974,

7. Sequences according to Claim 1 contained in the vpx gene of the viruses HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy23 : ATG TCA GAT CCC AGG GAG A
S, 5900-5918, 5813-5831,

MMy24 : CCT GGA GGG GGA GGA GGA GGA
AS, 6228-6208, 6141-6121,

8. Sequences according to Claim 1 contained in the env gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, these sequences being characterized by the following nucleotide sequences:

MMy5 : CCA ATT CCC ATA CAT TAT TGT GCC CC
S,6905-6930,6903-6928,6860-6885

MMy5.a : GGG GCA CAA TAA TGT ATG GGA ATT GG
AS, 6930-6905, 6928-6903, 6885-6860,
MMy6 : AAT GGC AGT CTA GCA GAA GAA GA
S,7055-7077,7053-7075,7010-7032
MMy7 : ATC CTC AGG AGG GGA CCC AGA AAT T
S, 7360-7384, 7349-7373,7306-7330
MMy7.a : AAT TTC TGG GTC CCC TCC TGA GGA T
AS, 7384-7360,7373-7349,7330-7306
MMy8 : GTG CTT CCT GCT GCT CCC AAG AAC CC
AS, 7857-7832,7846-7821,7800-7775
MMy8a : GGG TTC TTG GGA GCA GCA GGA AGC AC
S, 7832-7857, 7821-7846, 7775-7800,
MMy9 : ATG GGT GGC AAG TGG TCA AAA AGT AG
... ...A ... ...
S,8844-8869, 8836-8861, 8787-8812,
MMy9 a : CTA CTT TTT GAC CAC TTG CCA CCC AT
AS, 8869-8844, 8861-8836, 8812-8787,
MMy78 : TAT TAA CAA GAG ATG GTG G
S, 7629-7647, 7612-7630, 7572-7590,
MMy89 : CCA GCA AGA AAA GAA TGA A
S, 8224-8242, 8213-8231, 8167-8185,
MMy89 a . : TTC ATT CTT TTC TTG CTG G
AS, 8242-8224, 8231-8213, 8185-8167.

9. Sequences according to Claim 1 contained in the nef 1 gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-Eli, these sequences being characterized by the following nucleotide sequences:

MMy10 : AAA AGA AAA GGG GGG ACT GGA
S, 9116-9136, 9117-9137, 9062-9082,
MMy10a : TCC AGT CCC CCC TTT TCT TTT
AS,9136-9116, 9137-9117, 9082-9062,
MMy11 : AAA GTC CCC AGC GGA AAG TCC C
AS,9503-9483, 9505-9484, 9449-9428,

10. Sequences according to Claim 1 contained in the vif 1 gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, these sequences

being characterized by the following nucleotide sequences:

MMy15 : GAT TAT GGA AAA CAG ATG GCA GGT GAT
S, 5073-5099, 5068-5094, 5037-5063,
MMy16 : GCA GAC CAA CTA ATT CAT CTG TA
S, 5383-5405, 5378-5400, 5347-5369,
MMy16a : TAC AGA TGA ATT AGT TGG TCT GC
AS, 5405-5383, 5400-5378, 5369-5347,
MMy17 : CTT AAG CTC CTC TAA AAG CTC TA
AS, 5675-5653, 5670-5648, 5639-5617,

11. Sequences according to Claim 1 contained in the vpu gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy25 : GTA AGT AGT ACA TGT AAT GCA ACC T
S, 6081-6105, 6076-6100, 6045-6069,
MMy26 : AGC AGA AGA CAG TGG CCA TGA GAG
S, 6240-6263, 6238-6261, 6207-6230,
MMy27 : ACT ACA GAT CAT CAA TAT CCC AA
AS, 6343-6321, 6338-6316, 6307-6285,

12. Procedure for gene amplification of nucleotide sequences of viruses of the HIV-1 and/or HIV-2 and/or SIV type, performed starting from a biological sample, this procedure comprising mainly the following steps:

- a step involving the extraction of the nucleic acid to be detected belonging to the genome of the virus of the HIV-1, HIV-2 or SIV type possibly present in the above-mentioned biological sample and, where appropriate, a step involving treatment of the said nucleic acid with a reverse transcriptase if the former is in the form of RNA,
- a cycle comprising the following steps:

. denaturation of the double-stranded nucleic acid to be detected, which leads to the formation of a single-stranded nucleic acid,

. hybridization of each of the single-stranded nucleic acids

obtained during the preceding denaturation step with at least one primer according to one of the Claims 1 to 11, by placing the above-mentioned single-strands in contact with at least one of the above-mentioned primer couples,

. formation, starting from the primers, of the DNAs complementary to the single strands to which they are hybridized in the presence of a DNA polymerase and the four different nucleoside triphosphates (dNTPs), which leads to the formation of a greater number of double-stranded nucleic acids to be detected than at the preceding denaturation step, this cycle being repeated a specific number of times in order to obtain the said nucleic acid sequence to be detected possibly present in the biological sample in an amount sufficient to permit its detection,

- a step involving the detection of the possible presence of the nucleic acid belonging to the genome of the virus of the HIV-1 and/or HIV-2 and/or SIV type in the biological sample.

13. Procedure according to Claim 12, characterized in that the step involving the expression of the viral DNA comprises the following steps:

. suspension of the cell pellet in 0.5 ml of boiled water in a Potter homogenizer with a wide pestle,

. grinding of the cells by "forwards and backwards rotation",

. addition of Triton X100 to give a final concentration of 0.1%,

. heat denaturation for 15 to 25 minutes at 100°C,

. brief centrifugation in order to remove only the cell debris,

. precipitation of the DNA overnight at -20°C by the addition of 2.5 volumes of absolute ethanol and 10% of the final volume of 3 molar sodium acetate.

14. Procedure according to Claim 13, characterized in that the retro-transcription step of the viral RNA comprises the following steps:

- 10 µg of RNA, extracted and resuspended in water, are placed in the presence of the primer couple, each at a concentration of 0.8 µM, in a final volume of 40 µl; the mixture is denatured at 100°C for 10 minutes, then plunged into ice-cold water,

- 10 µl of the following mixture are added: 5 µl of the "10 X buffer" (containing, when it is diluted 1/10: Tris-HCl, pH = 8.9: 50 mM; $(NH_4)_2SO_4$: 15 mM; $MgCl_2$: 5 mM; ß-mercaptoethanol: 10 mM; gelatin: 0.25 mg/ml) + 1 unit of reverse transcriptase + 1 unit of Taq polymerase + 1 µl of a 25 mM mixture of each of the 4 dNTPs + water to give 10 µl; the synthesis of the cDNA results from the action of the reverse transcriptase at 42°C for 13 minutes, then the mixture is heated at 95°C for 3 minutes in order to destroy the reverse transcriptase.

15. Procedure according to one of the Claims 12 to 14, characterized in that the denaturation step is carried out in the presence of the primer couple(s) according to one of the Claims 1 to 11.

16. Procedure according to Claim 15, characterized in that it is performed under the following conditions:

- hybridization: the primers (1 µl of a 40 µmolar solution of each primer) are placed in the presence of the DNA-matrix (100 to 300 ng) for the first step of denaturation-reassociation; the tubes containing this mixture of DNA-matrix and primers are heated for 10 minutes at 100°C, then plunged into ice-cold water. The primers must be used at a final concentration of 0.8 µM each in the amplification step which follows.
- amplification: the 4 dNTPs, each being used at a concentration of 0.4 µmolar in the final solution (50 µl), and one unit of Taq polymerase per 50 µl of reaction mixture are added to the preceding mixture; this step is carried out in the amplification buffer designated by the name of "10 X buffer", the composition of which is given in Claim 14.

17. Use of the procedure according to any one of the Claims 12 to 16 for the in vitro diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type, or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV).

18. Use of the procedure according to any one of the Claims 12 to 16 for the amplification of nucleotide sequences of the genomes of the viruses of the HIV or SIV type, followed by the translation of these amplified sequences into proteins, starting from the nucleotide primers according to one of the Claims 1 to 11.

19. Immunogenic compositions containing one (or more) translation product of the nucleotide sequences according to one of the Claims 1 to 11, and/or one (or more) translation product of the nucleotide sequences amplified by the procedure according to one of the Claims 12 to 16.

20. The following oligonucleotide primer couples for the implementation of a method according to one of the Claims 12 to 16: MMy4Ba-MMy28a, MMy26-MMy5a, MMy8a-MMy89, MMy89a-MMy9a, MMy25-MMy27, MMy26-MMy27, MMy28-MMy29a, MMy29-MMy30a, MMy30-MMy31a, MMy31-MMy32a.

21. Kit for the implementation of a method according to one of the Claims 12 to 16 containing:
- at least one oligonucleotide primer couple according to any one of the Claims 1 to 11 or according to the Claim 20,
- suitable reagents for the implementation of a cycle of amplification operations, in particular DNA polymerase and the four different nucleotide triphosphates,
- 10 X buffer as described in Claim 14,
- one (or several) probe(s), which may be labelled, capable of hybridizing with the amplified nucleic acid sequence(s) to be detected.

22. Composition for the treatment of viral diseases, in particular AIDS, containing at least one anti-sense nucleotide sequence according to one of the Claims 1 to 11 in combination with a pharmaceutically acceptable vehicle.

23. Antibodies capable of giving rise to an immunological reaction with the translation products of the nucleotide sequences according to one of the Claims 1 to 11, and/or with one (or more) translation product(s) of the nucleotide sequences amplified by the method according to one of the Claims 12 to 16.

24. Method of <u>in vitro</u> diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type, or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV) comprising the placing of a biological sample (in particular serum) taken from a patient under study in contact with antibodies according to Claim 23, and the detection of the immunological complexes formed between the antigens of the viruses of the HIV or SIV type possibly present

in the biological sample and the said antibodies.

25. Kit for the implementation of a method according to Claim 24, containing antibodies according to Claim 23 and, where appropriate, suitable reagents for the detection of the immunological complex formed between the said antibodies and the antigens of the HIV and/or SIV viruses.

26. Buffer solution ("10 X buffer") for use in the hybridization step of the procedure according to Claim 12, or in the retrotranscription step of the viral RNA of the procedure according to Claim 14, characterized in that it is constituted, when diluted 1/10, of:

- Tris-HCl, pH 8.9: 50 mM;
- $(NH_4)_2SO_4$: 15 mM;
- $MgCl_2$: 5 mM;
- ß-mercaptoethanol: 10 mM;
- gelatin: 0.25 mg/ml.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Moncany, Maurice
Montagnier, Luc

(ii) TITLE OF INVENTION: Nucleotide Sequences Derived From The Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type, And Their Uses In Particular For The Amplification Of The Genomes Of These Retroviruses And For The In Vitro Diagnosis Of The Diseases Due To Those Viruses

(iii) NUMBER OF SEQUENCES: 68

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
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(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/160,465
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(vii) PRIOR APPLICATION DATA:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGCGCCCGA ACAGGGAC 18

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGCGCCTGA ACAGGGAC 18

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAGGGGG AAAGAAAAA 19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCCCGGCGG AAAGAAAAA 19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCCAGGAGG AAAGAAAAA 19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCCCATACA AAATGTTTTA 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCCCACACT ATATGTTTTA 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCATGGCTG CTTGATG 17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCATAGCTG CCTGGTG 17

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTTGCATGG CTGCTTGATG 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCTGCATAG CTGCCTGGTG 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CATCAAGCAG CCATGCAAAG 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCAGGCAG CTATGCAGAG 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGGGCTGTTG GAAATGTGG 19

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGGCTGTTG GAAAGGTGG 19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCACATTTCC AGCATCCCT 19

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACATTTCC AGCAGCCCT 19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCACATTTCC AGCACCCCT 19

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATAGATGGA ACAAGCCCCA G 21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCCATTTCTT GCTCTCCTCT GT 22

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAAAGCCAGG AATGGATGGC CCAA 24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAAAGCCAGG AATGGATGGA CCAA 24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGGCCATC CATTCCTGGC TTTA 24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTCCATC CATTCCTGGC TTTA 24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGGACTGTCA ATGACATACA GAA 23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGACTGTCA ATGATATACA GAA 23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCTGTATGT CATTGACAGT CCA 23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCTGTATGT CATTGACTGT CCA 23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATGGGTACC AGCACACAAA GG 22

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCTTTGTGTG CTGGTACCCA TG 22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGGAAAGGTG AAGGGGCAGT 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGAAAGGTG AAGGAGCAGT 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACTGCCCCTT CACCTTTCCA 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGCCCCTT CTCCTTTCCA 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACTGCCCCTT CCCCTTTCCA 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AGAGACTCTT GCGGGCGCGT G 21

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATATACTTAG AAAAGGAAGA AGG 23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCTTCTTCCT TTTCTAAGTA TAT 23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCTGAGACA GCAGGGACTT TCCA 24

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATGGAGGAG GAAAAGAGAT GGATAGT 27

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAGCACTTAT TTCCCTTGCT TT 22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAGCAAGGG AAATAAGTGC TA 22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCTTGTTCA TCATGCCAGT AT 22

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGTCAGATC CCAGGGAGA 19

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCTGGAGGGG GAGGAGGAGG A 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCAATTCCCA TACATTATTG TGCCCC 26

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGGCACAAT AATGTATGGG AATTGG 26

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AATGGCAGTC TAGCAGAAGA AGA 23

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCCTCAGGA GGGGACCCAG AAATT 25

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AATTTCTGGG TCCCCTCCTG AGGAT 25

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGCTTCCTG CTGCTCCCAA GAACCC 26

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGGTTCTTGG GAGCAGCAGG AAGCAC 26

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGTGGCA AGTGGTCAAA AAGTAG 26

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTACTTTTTG ACCACTTGCC ACCCAT 26

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TATTAACAAG AGATGGTGG 19

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CCAGCAAGAA AAGAATGAA 19

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCATTCTTT TCTTGCTGG 19

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAAGAAAAG GGGGGACTGG A 21

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TCCAGTCCCC CCTTTTCTTT T 21

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAAGTCCCCA GCGGAAAGTC CC 22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATTATGGAA AACAGATGGC AGGTGAT 27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCAGACCAAC TAATTCATCT GTA 23

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TACAGATGAA TTAGTTGGTC TGC 23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)